

#2

Karen 30

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/856,275

DATE: 06/12/2001

TIME: 10:58:36

Input Set : A:\Or5046u1.app

Output Set: N:\CRF3\06112001\I856275.raw

ENTERED

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3 <110> APPLICANT: Renard, Michel
4   Roscoe, Thomas James
5   Delseny, Michel
6   Bourgis, Fabienne
7   Barret, Pierre
8   Guerche, Philippe
9   Institut National de la Recherche Agronomique
10  Centre National de la Recherche Scientifique
11  Universite Pierre et Marie Curie
12  Universite Victor Segalen Bordeaux II
14 <120> TITLE OF INVENTION: Gene Coding for an Acyltransferase of Oil Seed Rape,
15   and Uses Thereof
17 <130> FILE REFERENCE: 45636-5046-US
C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/856,275
C--> 20 <141> CURRENT FILING DATE: 2001-05-18
22 <150> PRIOR APPLICATION NUMBER: FR 98/14470
23 <151> PRIOR FILING DATE: 1998-11-18
25 <150> PRIOR APPLICATION NUMBER: PCT/FR99/02827
26 <151> PRIOR FILING DATE: 1999-11-18
28 <160> NUMBER OF SEQ ID NOS: 3
30 <170> SOFTWARE: PatentIn Ver. 2.1
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1253
34 <212> TYPE: DNA
35 <213> ORGANISM: Brassica napus
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (58)..(1134)
40 <223> OTHER INFORMATION: Lysophosphatidic acyltransferase (LPAAT) gene
42 <220> FEATURE:
43 <221> NAME/KEY: variation
44 <222> LOCATION: (1253)
45 <223> OTHER INFORMATION: d = a or g or t.
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50 atg agc aaa tct cac gga cga tgt ttt agc tcg cga gat tcc gcc atg      105
51 Met Ser Lys Ser His Gly Arg Cys Phe Ser Ser Arg Asp Ser Ala Met
52   1           5           10           15
54 gat gtc gct tct gct cgg ggg gtc tcc tca cat cct cca tat tat agc      153
55 Asp Val Ala Ser Ala Arg Gly Val Ser Ser His Pro Pro Tyr Tyr Ser
56           20           25           30
58 aaa ccc att tgt tca tca cag tca tcg ttg att cgg att ccg atc agt      201
59 Lys Pro Ile Cys Ser Ser Gln Ser Ser Leu Ile Arg Ile Pro Ile Ser
60           35           40           45
62 aaa gga tgt tgc ttt gct cgt tct tcg aac ttg att act tcc ctt cat      249
63 Lys Gly Cys Cys Phe Ala Arg Ser Ser Asn Leu Ile Thr Ser Leu His
64           50           55           60

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66 gct gct tcg aga ggg gtg aca agg cgt act agt ggt gta caa tgg tgt 297
67 Ala Ala Ser Arg Gly Val Thr Arg Arg Thr Ser Gly Val Gln Trp Cys
68 65 70 75 80
70 tac cgt tct att aga ttt gac cct ttc aaa gtt aat gat aag aac tca 345
71 Tyr Arg Ser Ile Arg Phe Asp Pro Phe Lys Val Asn Asp Lys Asn Ser
72 85 90 95
74 aga act gtg act gtg aga tcg gat ctt tca gga gct gca acc cct gaa 393
75 Arg Thr Val Thr Val Arg Ser Asp Leu Ser Gly Ala Ala Thr Pro Glu
76 100 105 110
78 tct act tat cca gaa cca gag att aag ttg agc tca aga ctc aga ggg 441
79 Ser Thr Tyr Pro Glu Pro Glu Ile Lys Leu Ser Ser Arg Leu Arg Gly
80 115 120 125
82 ata tgc ttc tgt ctc gtt gct ggc atc tcc gcc att gtt ctc atc gtc 489
83 Ile Cys Phe Cys Leu Val Ala Gly Ile Ser Ala Ile Val Leu Ile Val
84 130 135 140
86 ctg atg atc att ggc cat ccc ttc gtc ctt cta ttt gat cgt tac agg 537
87 Leu Met Ile Ile Gly His Pro Phe Val Leu Leu Phe Asp Arg Tyr Arg
88 145 150 155 160
90 aga aag ttc cat cac ttc att gct aag ctt tgg gct tcc ata agc atc 585
91 Arg Lys Phe His Phe Ile Ala Lys Leu Trp Ala Ser Ile Ser Ile
92 165 170 175
94 tac ccg ttt tac aaa aca gac atc caa ggt ttg gag aat ctg ccg tcg 633
95 Tyr Pro Phe Tyr Lys Thr Asp Ile Gln Gly Leu Glu Asn Leu Pro Ser
96 180 185 190
98 tca gac act cct tgt gta tac gtt tcg aac cac caa agc ttt ctg gat 681
99 Ser Asp Thr Pro Cys Val Tyr Val Ser Asn His Gln Ser Phe Leu Asp
100 195 200 205
102 ata tac aca ctt ctc agc ctt ggc caa agc tat aag ttc atc agc aag 729
103 Ile Tyr Thr Leu Leu Ser Leu Gly Gln Ser Tyr Lys Phe Ile Ser Lys
104 210 215 220
106 aca ggg ata ttc gtt att cct gtc atc ggt tgg gct atg tcc atg atg 777
107 Thr Gly Ile Phe Val Ile Pro Val Ile Gly Trp Ala Met Ser Met Met
108 225 230 235 240
110 ggg gtt gtt ccc ttg aag agg atg gac cca aga agc caa gtg gat tgc 825
111 Gly Val Val Pro Leu Lys Arg Met Asp Pro Arg Ser Gln Val Asp Cys
112 245 250 255
114 tta aaa cgc tgc atg gaa cta gtg aag aag gga gct tcc gtc ttt ttc 873
115 Leu Lys Arg Cys Met Glu Leu Val Lys Lys Gly Ala Ser Val Phe Phe
116 260 265 270
118 ttc cca gag gga acg agg agt aag gat ggt cgg tta ggt cct ttc aag 921
119 Phe Pro Glu Gly Thr Arg Ser Lys Asp Gly Arg Leu Gly Pro Phe Lys
120 275 280 285
122 aaa ggg gct ttt acg ata gca gct aag aca gga gtt cca gtg gtg cca 969
123 Lys Gly Ala Phe Thr Ile Ala Ala Lys Thr Gly Val Pro Val Val Pro
124 290 295 300
126 ata acg ctg atg gga aca ggg aag atc atg ccg acg ggt agt gaa ggt 1017
127 Ile Thr Leu Met Gly Thr Gly Lys Ile Met Pro Thr Gly Ser Glu Gly
128 305 310 315 320
130 ata ctg aat cat ggg gat gtg aga gtg atc atc cac aag ccg ata tat 1065

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131 Ile Leu Asn His Gly Asp Val Arg Val Ile Ile His Lys Pro Ile Tyr
132           325           330           335
134 gga agc aaa gct gat gtt ctt tgc gaa gag gcg aga aac aag ata gct 1113
135 Gly Ser Lys Ala Asp Val Leu Cys Glu Glu Ala Arg Asn Lys Ile Ala
136           340           345           350
138 gaa tct atg aat ctc ttg agt tgaacgttt gttttttaag cagtgtctct 1164
139 Glu Ser Met Asn Leu Leu Ser
140           355
142 atgaacaatg agaaggctaa accatttttta catgtcagtt ttattgttta aaataaaaatt 1224
144 taggcttttc aaaaaaaaaa aaaaaaaad 1253
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 359
149 <212> TYPE: PRT
150 <213> ORGANISM: Brassica napus
152 <400> SEQUENCE: 2
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154 1 5 10 15
156 Asp Val Ala Ser Ala Arg Gly Val Ser Ser His Pro Pro Tyr Tyr Ser
157 20 25 30
159 Lys Pro Ile Cys Ser Ser Gln Ser Ser Leu Ile Arg Ile Pro Ile Ser
160 35 40 45
162 Lys Gly Cys Cys Phe Ala Arg Ser Ser Asn Leu Ile Thr Ser Leu His
163 50 55 60
165 Ala Ala Ser Arg Gly Val Thr Arg Arg Thr Ser Gly Val Gln Trp Cys
166 65 70 75 80
168 Tyr Arg Ser Ile Arg Phe Asp Pro Phe Lys Val Asn Asp Lys Asn Ser
169 85 90 95
171 Arg Thr Val Thr Val Arg Ser Asp Leu Ser Gly Ala Ala Thr Pro Glu
172 100 105 110
174 Ser Thr Tyr Pro Glu Pro Glu Ile Lys Leu Ser Ser Arg Leu Arg Gly
175 115 120 125
177 Ile Cys Phe Cys Leu Val Ala Gly Ile Ser Ala Ile Val Leu Ile Val
178 130 135 140
180 Leu Met Ile Ile Gly His Pro Phe Val Leu Leu Phe Asp Arg Tyr Arg
181 145 150 155 160
183 Arg Lys Phe His His Phe Ile Ala Lys Leu Trp Ala Ser Ile Ser Ile
184 165 170 175
186 Tyr Pro Phe Tyr Lys Thr Asp Ile Gln Gly Leu Glu Asn Leu Pro Ser
187 180 185 190
189 Ser Asp Thr Pro Cys Val Tyr Val Ser Asn His Gln Ser Phe Leu Asp
190 195 200 205
192 Ile Tyr Thr Leu Leu Ser Leu Gly Gln Ser Tyr Lys Phe Ile Ser Lys
193 210 215 220
195 Thr Gly Ile Phe Val Ile Pro Val Ile Gly Trp Ala Met Ser Met Met
196 225 230 235 240
198 Gly Val Val Pro Leu Lys Arg Met Asp Pro Arg Ser Gln Val Asp Cys
199 245 250 255
201 Leu Lys Arg Cys Met Glu Leu Val Lys Lys Gly Ala Ser Val Phe Phe
202 260 265 270

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204 Phe Pro Glu Gly Thr Arg Ser Lys Asp Gly Arg Leu Gly Pro Phe Lys
205           275           280           285
207 Lys Gly Ala Phe Thr Ile Ala Ala Lys Thr Gly Val Pro Val Val Pro
208           290           295           300
210 Ile Thr Leu Met Gly Thr Gly Lys Ile Met Pro Thr Gly Ser Glu Gly
211 305           310           315           320
213 Ile Leu Asn His Gly Asp Val Arg Val Ile Ile His Lys Pro Ile Tyr
214           325           330           335
216 Gly Ser Lys Ala Asp Val Leu Cys Glu Glu Ala Arg Asn Lys Ile Ala
217           340           345           350
219 Glu Ser Met Asn Leu Leu Ser
220           355
224 <210> SEQ ID NO: 3
225 <211> LENGTH: 7
226 <212> TYPE: PRT
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
231     sequence of LPAATs
233 <220> FEATURE:
234 <221> NAME/KEY: VARIANT
235 <222> LOCATION: (3)..(6)
236 <223> OTHER INFORMATION: Xaa can be any amino acid.
238 <400> SEQUENCE: 3
W--> 239 Asn His Xaa Xaa Xaa Xaa Asp
240    1           5

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VERIFICATION SUMMARY

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L:19 M:270 C: Current Application Number differs, Replaced Application Number
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3